STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/686,490C
Source: IFW0
Date Processed by STIC: 2/25/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED | **SUGGESTED CORRECTION** | **SERIAL NUMBER:** 10/686,490C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C TIME: 10:06:06

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

see item 4 on Error Summary Sheet

pp 2,4

Does Not Comply
Corrected Diskette Needed

```
     3 <110> APPLICANT: Bayer Aktiengesellschaft
     4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
     5 <130> FILE REFERENCE: LeA 35 991
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/686,490C
C--> 6 <141> CURRENT FILING DATE: 2003-10-15
     6 <160> NUMBER OF SEQ ID NOS: 2
     7 <170> SOFTWARE: PatentIn version 3.1
     9 <210> SEQ ID NO: 1
    10 <211> LENGTH: 885
    11 <212> TYPE: DNA
    12 <213> ORGANISM: unknown
    13 <220> FEATURE:
    14 <221> NAME/KEY: CDS
    15 <222> LOCATION: (1)..(885)
    16 <223> OTHER INFORMATION: bacterial
    18 <400> SEQUENCE: 1
    19 atg gca cag gtg aag gcc aac ggc att acc ctc gag tat gaa gag cag      48
    20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
    21 1               5                  10                  15
    23 ggc cat cgc cac cat ccg tcc atg ctc ctc att atg ggc ctg ggc ggc      96
    24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
    25             20                  25                  30
    27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga     144
    28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
    29         35                  40                  45
    31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac gcg ggg ctt tcg acg     192
    32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
    33     50                  55                  60
    35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctc ctg     240
    36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
    37 65                  70                  75                  80
    39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctc gac gac atg     288
    40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
    41                 85                  90                  95
    43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc     336
    44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
    45             100                 105                 110
    47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg     384
    48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
    49         115                 120                 125
    51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc     432
    52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
    53     130                 135                 140
```

```
     55 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag      480
     56 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
     57 145                 150                 155                 160
     59 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac      528
     60 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
     61                 165                 170                 175
     63 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag      576
     64 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
     65             180                 185                 190
     67 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc      624
     68 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
     69         195                 200                 205
     71 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg      672
     72 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
     73     210                 215                 220
     75 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg      720
     76 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
     77 225                 230                 235                 240
     79 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac      768
     80 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
     81                 245                 250                 255
     83 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac      816
     84 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
     85             260                 265                 270
     87 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac      864
     88 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
     89         275                 280                 285
     91 gcc gcg gcc gcg gaa gct taa                                       885
     92 Ala Ala Ala Ala Glu Ala
     93     290
     96 <210> SEQ ID NO: 2
     97 <211> LENGTH: 294
     98 <212> TYPE: PRT
     99 <213> ORGANISM: unknown
W--> 102 <220> FEATURE:
W--> 102 <223> OTHER INFORMATION: bacterial
W--> 102 <400> 2
    104 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
    105 1               5                   10                  15
    108 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
    109             20                  25                  30
    112 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
    113         35                  40                  45
    116 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
    117     50                  55                  60
    120 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
    121 65                  70                  75                  80
    124 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
    125                 85                  90                  95
```

see p. 4 for explanation

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

```
128 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
129             100                 105                 110
132 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
133         115                 120                 125
136 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
137     130                 135                 140
140 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
141 145                 150                 155                 160
144 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
145                 165                 170                 175
148 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
149             180                 185                 190
152 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
153         195                 200                 205
156 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
157     210                 215                 220
160 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
161 225                 230                 235                 240
164 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
165                 245                 250                 255
168 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
169             260                 265                 270
172 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
173         275                 280                 285
176 Ala Ala Ala Ala Glu Ala
177     290
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C TIME: 10:06:07

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

not explanatory

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2

VERIFICATION SUMMARY DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C TIME: 10:06:07

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:102 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213> ORGANISM:unknown
L:102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213> ORGANISM:unknown
L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:102